

Amendments to the Claims

1. (Currently Amended) An isolated and purified bacterial reverse transcriptase (RT) of (SEQ ID NO: 1), which synthesizes msDNA, and ~~which~~ wherein said RT reverse transcriptase further comprises:

1) a sequence of amino acid residues as follows: Tyr-Xaa₆-Asp-Asp of (SEQ ID NO: 50), wherein Xaa₆ is alanine or cysteine;

2) and further comprises a second sequence of amino acid residues as follows: Asn-Xaa₁-Xaa₂, wherein Xaa₁ is a hydrophobic residue selected from the group consisting of alanine, leucine, ~~and or~~ phenylalanine, and Xaa₂ is a hydrophobic residue selected from the group consisting of leucine, valine, ~~and or~~ isoleucine[.];

3) a third sequence of amino acid residues as follows: Ser-Xaa₃-Xaa₄-Xaa₅ of SEQ ID NO: 51, wherein Xaa₃ is a hydrophobic residue selected from the group consisting of valine, phenylalanine, leucine, or isoleucine, Xaa₄ is a polar residue selected from the group consisting of threonine, asparagine, lysine, or serine, and Xaa₅ is a hydrophobic residue selected from the group consisting of tryptophan, phenylalanine, or alanine;

4) a fourth sequence of amino acid residues as follows: Xaa₇-Val-Thr-Gly, wherein Xaa₇ is a polar residue selected from the group consisting of arginine, glutamic acid, valine, or glutamine, of SEQ ID NO: 52; and

5) a fifth sequence of amino acid residues as follows: Gly-Xaa₈-Pro, wherein Xaa₈ is selected from the group consisting of alanine, phenylalanine or serine.

2. – 4. (Canceled)

5. (Currently Amended) The bacterial RT-reverse transcriptase of claim 1 ~~which has the common subdomains 1 through 7 in Figure 14, which sequences are shown comprising an amino acid sequence selected from the group consisting of SEQ ID Nos~~NO.: ~~32, 33, 34, 35, 37, and SEQ ID NO.:~~ 32, 33, 34, 35, 37, and SEQ ID NO.: 38.

6. (Canceled)

7. (Currently Amended) An isolated and purified bacterial reverse transcriptase (RT) which synthesizes msDNA and which is essential for the synthesis of msDNA *in vivo*, said RT comprises a sequence of amino acid residues as follows: Tyr- Xaa₆-Asp-Asp of SEQ ID NO.: 50, wherein Xaa₆ is alanine or cysteine, ~~as shown in SEQ ID NO: 50~~, wherein said sequence is located in subdomain 5 shown in Fig. 14 at positions 175-191 of SEQ ID NO: 32, at positions 175-191 of SEQ ID NO: 33, at positions 175-191 of SEQ ID NO: 34, at positions 168-184 of SEQ ID NO: 35, at positions 159-175 of SEQ ID NO: 36, at positions 171-187 of SEQ ID NO: 37, and at positions 157-173 of SEQ ID NO: 38, and further comprising the 61 amino acid residues ~~as shown~~ indicated by black dots in the consensus sequence shown in Figure 14 of SEQ ID Nos: 32-28, wherein h is a hydrophobic residue and p is a small polar residue.

8. – 11. (Canceled)

12. (Currently Amended) The isolated and purified RT-reverse transcriptase of claim ~~[[4]]~~ 1 having an N-terminus and a C-terminus, which RT-reverse transcriptase has in the following order ~~starting from the N-terminus~~ to the C-terminus:

(1) ~~an a first amino acid sequence of Ser-Xaa₃-Xaa₄-Xaa₅-(SEQ ID NO:51)~~, wherein Xaa₃ is ~~a hydrophobic residue selected from the group consisting of valine, phenylalanine,~~

leucine, and or isoleucine, Xaa₄ is a polar residue selected from the group consisting of threonine, asparagine, lysine, and or serine, and Xaa₅ is a hydrophobic residue selected from the group consisting of tryptophan, phenylalanine, and or alanine;

(2) a second amino acid sequence Gly-Xaa₈-pro, wherein Xaa₈ is alanine, phenylalanine or serine;

(23) an a third amino acid sequence of Asn-Xaa₁-Xaa₂, where wherein Xaa₁ is a hydrophobic residue selected from the group consisting of alanine, leucine, and or phenylalanine, and Xaa₂ is a hydrophobic residue selected from the group consisting of leucine, valine, and or isoleucine;

(34) an a fourth amino acid sequence Tyr-Xaa₆-Asp-Asp (SEQ ID NO:50) wherein Xaa₆ is a alanine or cysteine; and

([[4]]5) an amino acid, Xaa₇, where Xaa₇ is a polar residue selected from the group consisting of arginine, lysine, glutamic acid, glutamine, and valine; a fifth amino acid sequence Xaa₇-Val-Thr-Gly, wherein Xaa₇ is arginine, glutamic acid, valine or glutamine.

13-16 (Canceled)

17. (Currently Amended) The isolated and purified bacterial reverse transcriptase (RT) of claim 1 having an N-terminus and a C-terminus, which RT reverse transcriptase has in the following order starting from the N-terminus to the C-terminus; an

a first amino acid sequence of Asn-Xaa₁-Xaa₂, where Xaa₁ is a hydrophobic residue selected from the group consisting of alanine, leucine and or phenylalanine and Xaa₂ is a hydrophobic residue selected from the group consisting of leucine, valine and or isoleucine;

an a second amino acid sequence of Ser-Xaa₃-Xaa₄-Xaa₅ (SEQ ID NO:51), wherein Xaa₃ is a hydrophobic residue selected from the group consisting of valine, phenylalanine,

~~leucine and or isoleucine, Xaa₄ is a polar residue selected from the group consisting of~~
~~threonine, asparagine, lysine and or serine, and Xaa₅ is a hydrophobic residue selected from the~~
~~group consisting of tryptophan, phenylalanine and or alanine;~~ an

a third amino acid sequence of Tyr-Xaa₆-Asp-Asp (SEQ ID NO: 50), where
Xaa₆ is ~~a~~ alanine or cysteine, ~~;~~ an and

a fourth amino acid sequence of Xaa₇-Val-Thr-Gly (SEQ ID NO: 52), where
Xaa₇ ~~is a polar residue selected from the group consisting of arginine, lysine, glutamic acid,~~
~~glutamine and or valine.~~

18. (New) The isolated and purified bacterial reverse transcriptase of claim 1,
wherein said reverse transcriptase is derived from *Myxococcus xanthus* or *Escherichia coli*.